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Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramateu, M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK049639
2514 bp mRNA linear HTC 03-APR-2004 Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:5530010015 product:GLYPICAN-2 PRECURSOR (CEREBROGLYCAN) (HSPG M13) homolog [Rattus norvegicus], full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okacaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
             BX44974 BX444974
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CN347353 170006000
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Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK049639
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HTC, CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Gangolli, E.A., Spytek, K.A., Gilbert, J., Casman, S., Blalock, A., Li, L., Vernet, C.A., Shenoy, S., Mishra, V., Furtak, K., Gerlach, V., Edinger, S., Malyankar, U., Stone, D., Millet, I., Smithson, G., Gunther, B., Padigaru, M., Taupier, R.J. and Anderson, D. Human proteins, polynucleotides encoding them and methods of using
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Curagen Corporation (US)
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Sequence 19 from Patent WO02055702.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX661917
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AX096281 Homo sapi
BC027972 Homo sapi
AL634418 Homo sapi
AX600207 Sequence
AX661921 Sequence
AX661919 Sequence
AX661919 Sequence
AX093588 Homo sapi
AX661923 Sequence
AY093588 Homo sapi
AX661923 Sequence
AR105268 Mus muscu
BD018231 Novel gen
                                                                         November 21, 2004, 18:53:50; Search time 5046 Seconds (without alignments)
16728.520 Million cell updates/sec
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Sequence
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AX937190 S
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           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                       4526729 segs, 23644849745 residues
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RATCRBGLVC
                                                    - nucleic search, using sw model
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Maximum Match 1008
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Maximum DB seq length: 200000000
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69.0 1613
63.8 1976
40.9 2135
20.1 3515
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PAT 22-MAR-2003

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X83577 M. musculus CQ718474 Sequence BC062902 Wus muscu AF485613 Mus muscu BC017166 Homo sapi AK252490 Sequence AX092292 Sequence AX376068 Sequence AX37607 Homo sapi CQ715188 Sequence

CQ767641 Sequence AX356462 Homo sapi AF111178 Homo sapi AX020118 Sequence AF105267 Homo sapi CQ782670 Sequence BD127255 Primer fo AK074741 Homo sapi AC092483 Homo sapi

AX020122 Sequence X54232 Human mRNA

BC023448 Mus muscu BC006622 Mus muscu

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November 21, 2004, 18:47:40; Search time 601 Seconds (without alignments)
15591.043 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                4134886 seqs, 2624710521 residues
                                                                - nucleic search, using sw model
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seq length: 200000000
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Sequence:
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Maximum DB
                                                                  OM nucleic
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:* geneseqn2003ds:* geneseqn2003as:* geneseqn2003bs:*

geneseqn20048:*

Abs78649 Human CDN Add49106 Human NOV Add49098 Human NOV Add4909 Human NOV Add49104 Human NOV Abs51686 DNA encod Add49092 Human NOV Add49109 Human NOV Add49109 Human NOV Add49109 Human NOV Add49096 Human NOV Add49096 Human NOV Add49096 Human NOV Abz59274 Human ROV Abz59274 Human ROV Abz59274 Human ROV Abz71193 Novel hum Abv71181 Novel hum Abs51684 DNA encod Add49088 Human NOV Adm02499 Human cDN Abz59273 Human GPC Aah30728 Human col Abs51687 DNA encod Description SUMMARIES ADD49098 ADD49090 ADD49104 ABS51686 ADD49106 ADD49086 ADD49094 ADD49096 ABZ59274 ABZ59273 AAH30728 ABS51687 ADD49100 ABS51684 2 2 2220 22 Query Match Length DB 1648 100.0 100.0 99.6 41.0 40.9 27.2 20.9 20.1 97.0 90.8 88.3 81.4 63.8 63.8 63.0 43.0 730.4 485.4 373.8 358.8 Score 1737.4 1730.6 1730.6 1621.4 1575.6 1453.4 1153.4 732 Result 22987654321098765

Add49102 Human NOV Ado07731 Mouse pol Aa194394 Human neu Aa194394 Human neu	Aad08307 Human sec Aad08284 Human sec Aad54707 Human olv	Addf33593 Haematopo Add07726 Human pol	Abx76377 Lung canc Abx59272 Human GPC	Acc72657 Human gly Adn39701 Cancer/an	Adn38929 Cancer/an Adq19916 Human sof	3 Human Human	Human		Aca73432 Human sec Aca05747 Human sec
ADD49102 ADO07731 AA194394 AA194393	AAD08307 AAD08284 AAD54707	ADF53593 AD007726	ABX76377 ABZ59272	ACC72657 ADN39701	ADN38929 ADQ19916	ABZ59283 AAZ33983	AAC78482 AAS45972	ACA89422	ACA05747
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20.1 19.1 18.8	18.3 18.3	1.81	18.1	18.1 18.1	18.1 18.1	17.8	17.8	17.8	17.8
358.8 334.8 332.4	326 326 323	323 323 323	323	323 323	323 323	318.2	318.2	318.2	318.2
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ALIGNMENTS

RESULT 1 ABS51684

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: genesequidates:
2: genesequidates:
3: genesequidous:
4: genesequidous:
5: genesequidous:

geneseqn2002as:* geneseqn2002bs:*

N_Geneseq_233ep04:*

Database

Human; NOVX; pathological condition; NOVX-associated disorder;
Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder;
renal artery stenosis; interstitial nephritis; glomerulonephritis;
polycystic kidney disease; cararact; Alzhaimar's disease; cancer;
acoustic trauma; cardiomyopathy; atherosclerosis; hypertension;
congenital heart defect; scleroderma; endometriosis; heemophilia;
dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy;
multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis;
ene; wound; askina; human disease; calpain; epsin; synaptotagmin;
low density lipoprotein B; LDLB; purinoceptor; CG8841; synaptotagmin;
serine protease TLSP; mitogen activated protein kinase kinase-2;
glypican-2 precursor; thymosin beta-10; gene; ds. DNA encoding human Glypican-2 Precursor-like protein #1. ABS51684 standard; DNA; 1785 BP (first entry) Homo sapiens 05-NOV-2002

WO200255702=N3. Com 18-JUL-2002 26-Der-2001; 2001WO-US050925

26-OCT-2000; 2000US-0243522P. 26-OCT-2000; 2000US-0243642P. 27-OCT-2000; 2000US-024361P. 27-OCT-2000; 2000US-0244443P. 31-OCT-2000; 2000US-0244443P. 01-NOV-2000; 2000US-024495P. 2000US-0244443P. 2000US-0244995P. 2000US-0245029P. 2000US-0245293P. 26-OCT-2000; 02-NOV-2000;

2000US-0245315P.

2001US-0262994P